


“Interesting and *new for their site*”

-Valentina

# Community-driven Interface Development

# Suddenly, it hit me

- I  H.C.I. studies
- My programmer does not actually know what the community wants.
  - make tools, get excited by tools, show-case those tools
- It is unlikely that each clade-specific community will be the same.

# It's the community, Stupid

For each clade:

- ***Phase 1 : Subjective assessment***
  - Find the scientific community (3 mo)
- ***Phase 2 : Design and refinement***
  - Solicit the scientific community (2 mo)
- ***Phase 3 : Performance assessment***
  - Evaluate if they are happy (1 mo)
- **Repeat**
  - (forever)

# Personnel

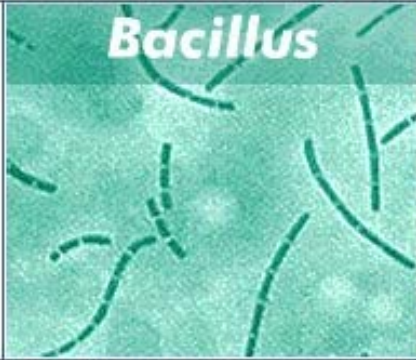
- Project Coordinator (Lauren)
- Per clade:
  - Assign Contact Bioinformatics Analyst
  - Assign Contact Bioinformatics Engineer



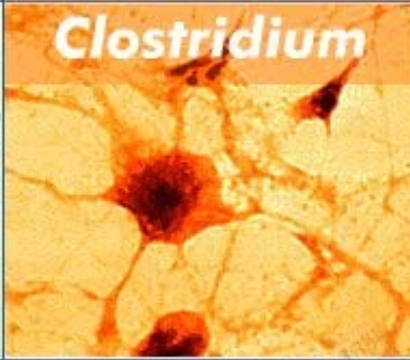
# Pathema

Bioinformatics Resource Center

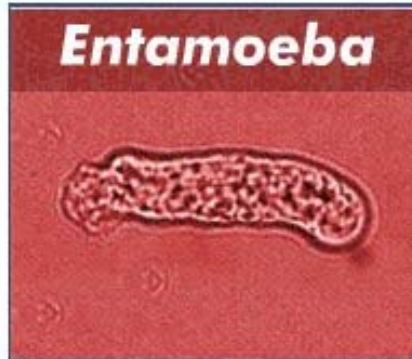
**Bacillus**



**Clostridium**



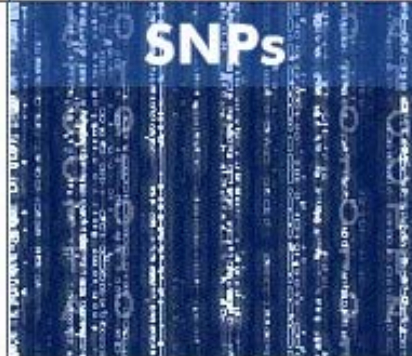
**Entamoeba**



**Burkholderia**



**SNPs**



“your baby is always beautiful”



## Genomes Available

- + [Burkholderia mallei](#) (7)
- + [Burkholderia pseudomallei](#) (7)

## Highlighted Tools

- Genomes to be sequenced
- Strain & DNA availability
  - BEI Resources
    - Acquire resources from BEI
    - Deposit resources at BEI
    - Search BEI for resources
- + Virulence factors
- Protocols
  - TIGR Annotation SOPs
  - Gene Prediction
  - Homology Searches
  - Automated Annotation
  - Manual Curation
  - Overlaps
  - Start Site Curation
  - Short ORF
  - Frameshift
  - Submit protocols to Pathema
- Microarrays
  - PFGRC
    - [Burkholderia](#) microarray
    - Microarray request process
- [Burkholderia](#) gene lists

## Google™ Search

- ☐ Search pathema.tigr.org
- ☐ Search the www

## Welcome to the Pathema *Burkholderia* Resource

As an [NIAID Bioinformatics Resource Center](#) (BRC) Pathema contains in depth curatorial analysis of six target organisms from the list of [NIAID category A-C pathogens](#). Pathema also offers single-genome and comparative multi-genome analyses as well as display tools at the genome, gene, and pathway level for these pathogens.

### Pathema Menu Bar Tools

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Search Pathema for genes, genomes, sequence regions, and evidence.

#### Genome Tools

Find organism lists as well as summary information and analyses for selected genomes.

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Compare multiple genomes based on a variety of criteria, including sequence homology and gene attributes. SNP data is also found under this menu.

#### Lists

Select and download gene, evidence, and genomic element lists.

#### Downloads

Download gene sequences or attributes for Pathema organisms, or go to our FTP site.

#### Carts

Select genome preferences from our Genome Cart or download your Gene Cart genes.

#### Organism Menu

See all available Pathema genomes from the Organism Menu at the top of each page.

### Additional Resources

- |   |  |   |                                 |
|---|--|---|---------------------------------|
| ♦ <a href="#">BRC Central</a>             | ♦ <a href="#">Reactome</a>                         | ♦ <a href="#">Botulinum Neurotoxin Resource</a> | ♦ <a href="#">Anthrax Resou</a> |
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| ♦ <a href="#">TIGR Annotation SOPs</a>    | ♦ <a href="#">TIGR Gene Naming Conventions</a>     | ♦ <a href="#">Explanation of Terms</a>          | ♦ <a href="#">TIGR Role Ids</a> |
| ♦ <a href="#">Pathema Mailing List</a>    | ♦ <a href="#">Description of all Pathema Tools</a> | ♦ <a href="#">Pathema Data Release Control</a>  |                                 |

## Announcements

### Latest Releases

Data Release: [4.0](#)  
Website Version: [2.1](#)

### News

[July 14, 2006](#): Website Version 2.1 has been released with additional SNP tools, [Reactome displays](#), and transporter data. View our [tutorial](#) to learn more about navigation on the redesigned site.

### Presentations

- ♦ TIGR: [Aug 8-10, 2006](#)
- ♦ TIGR: [Oct 10-12, 2006](#)
- ♦ Baltimore: [Oct 28-31, 2006](#)

# Phase 1: Subjective assessment

## **Identify targets:**

**axe TIGR faculty - Contact BA**

**compile email list**

**contact authors**

**Create online survey**

**Email and track survey lists**

**Correlate results**



# Phase 2: Design and Refinement

**Coordinate w/ web development team**

**Design Prototype**

**Consolidate literature and data**

**Epidemiology literature**

**IEDB collaboration**

**update new characterized tables**

**curate data dump of genus specific characterizations**

**update with additional characterizations**

**Data storage**

**organism specific database**

**implement characterized tables**

**Gemina database**

# **Phase 3 : Performance assessment**

## **Tool development**

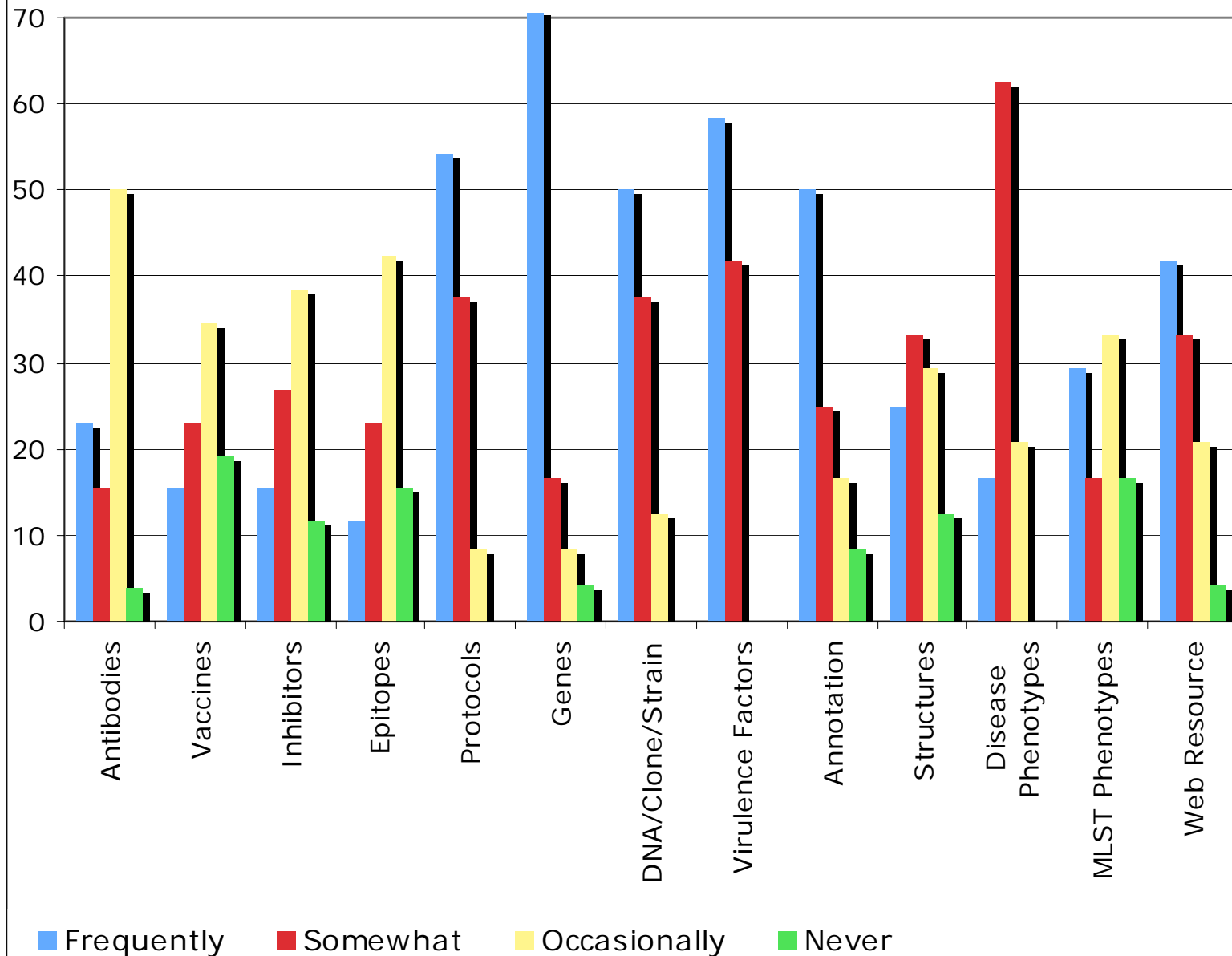
**Coordinate w/ web development team**

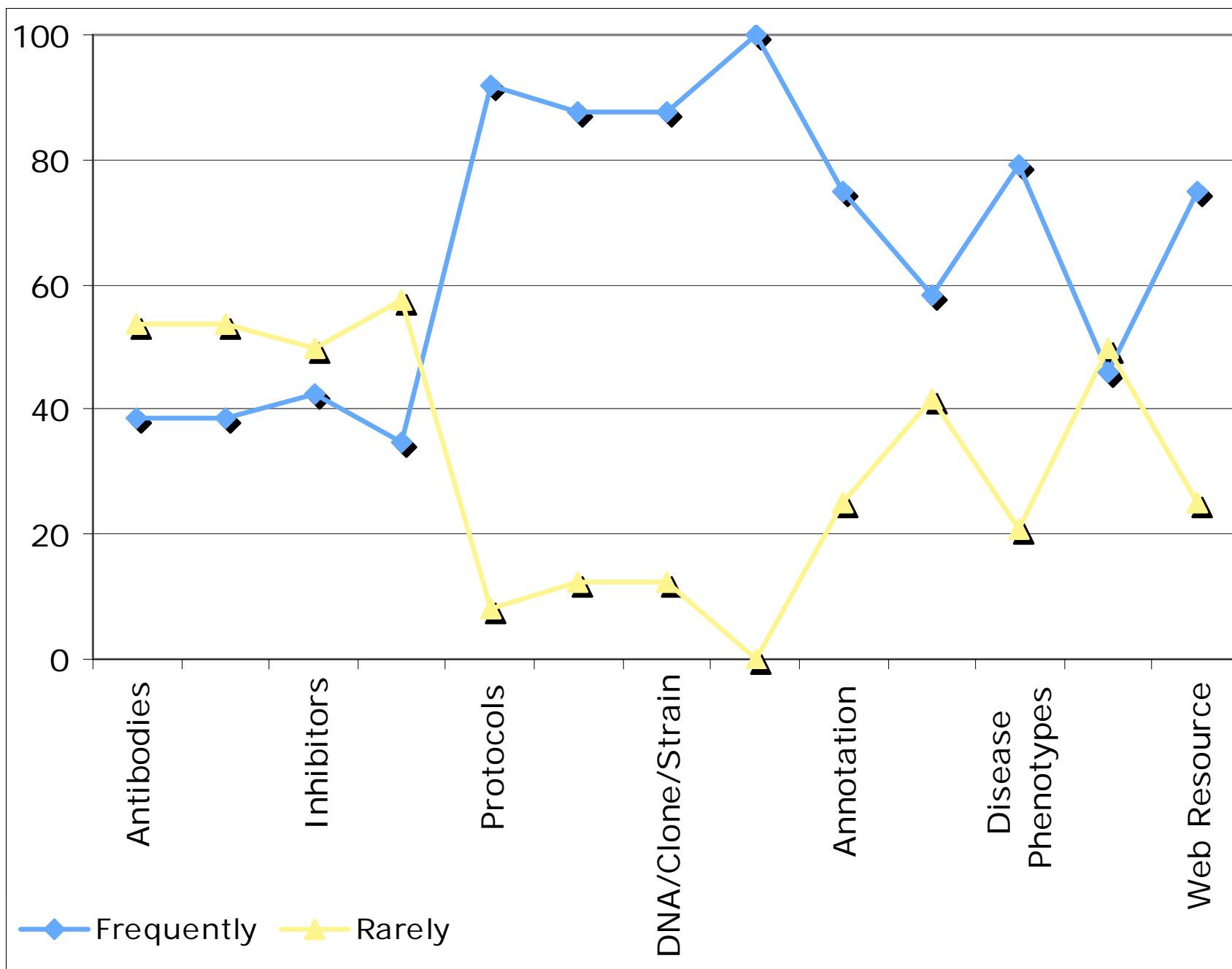
**Continue to consolidate literature and data**

**Continual solicitation of community editorial/usage feedback**

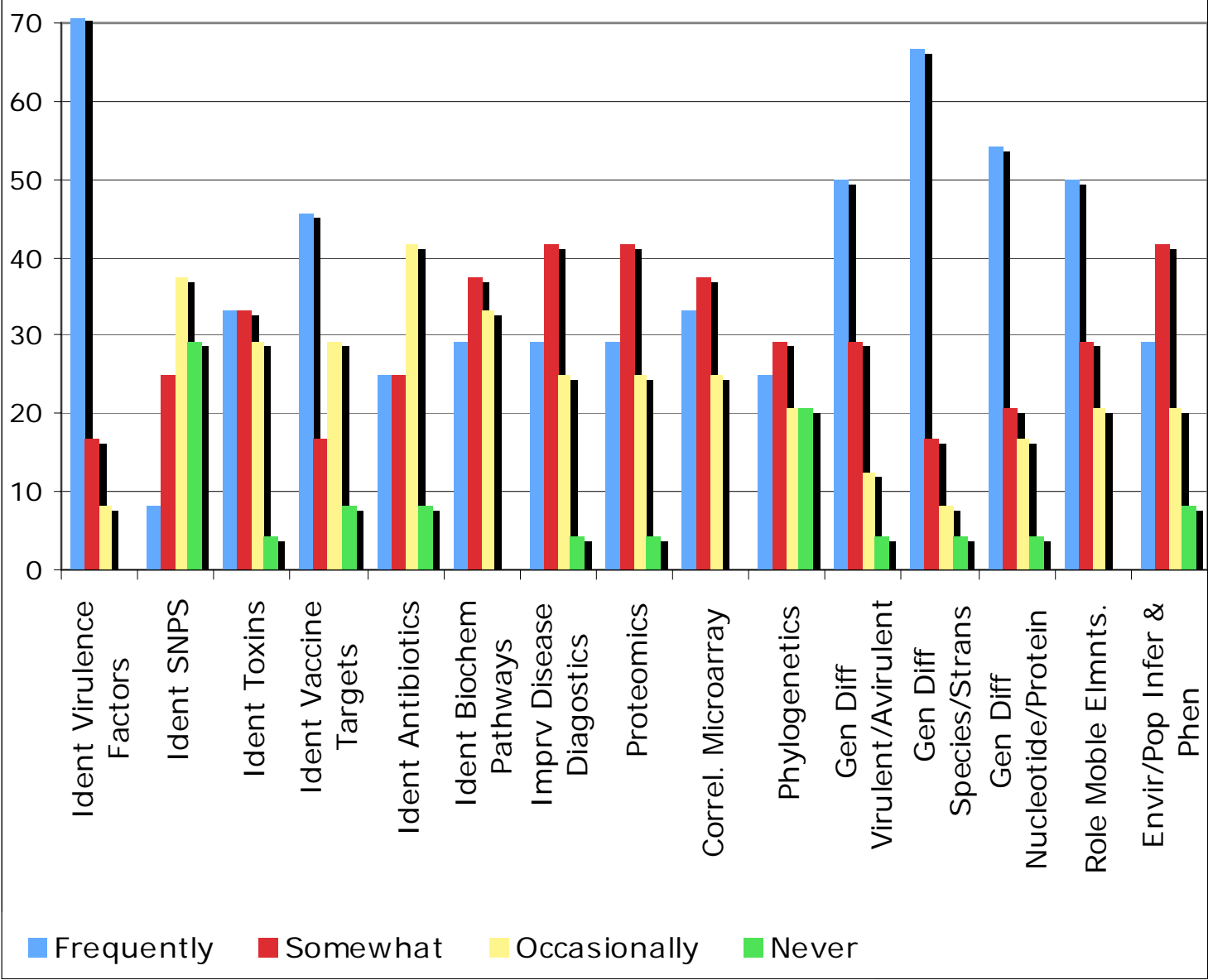
# Burkholderia Research Interests

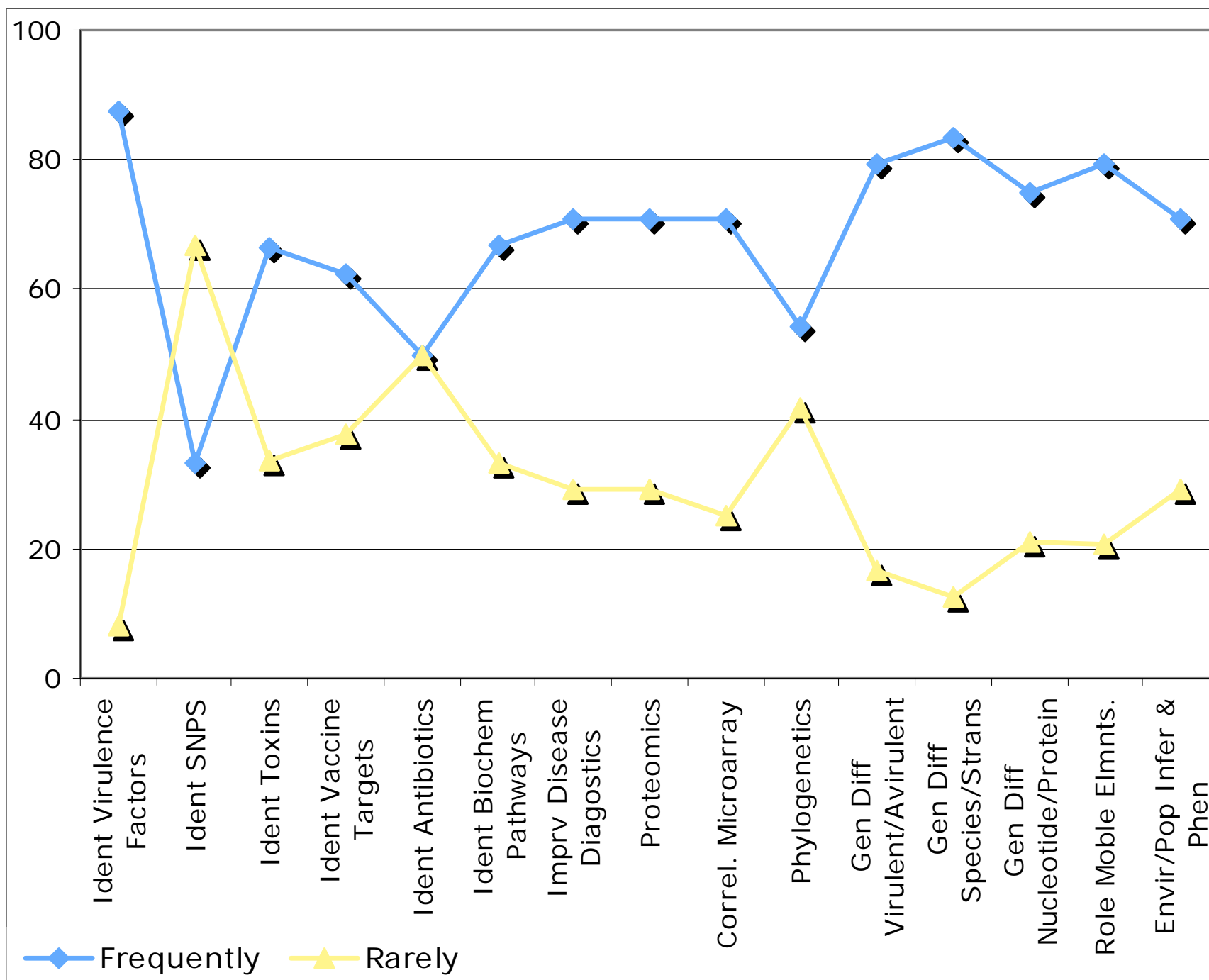
## 29 Respondents



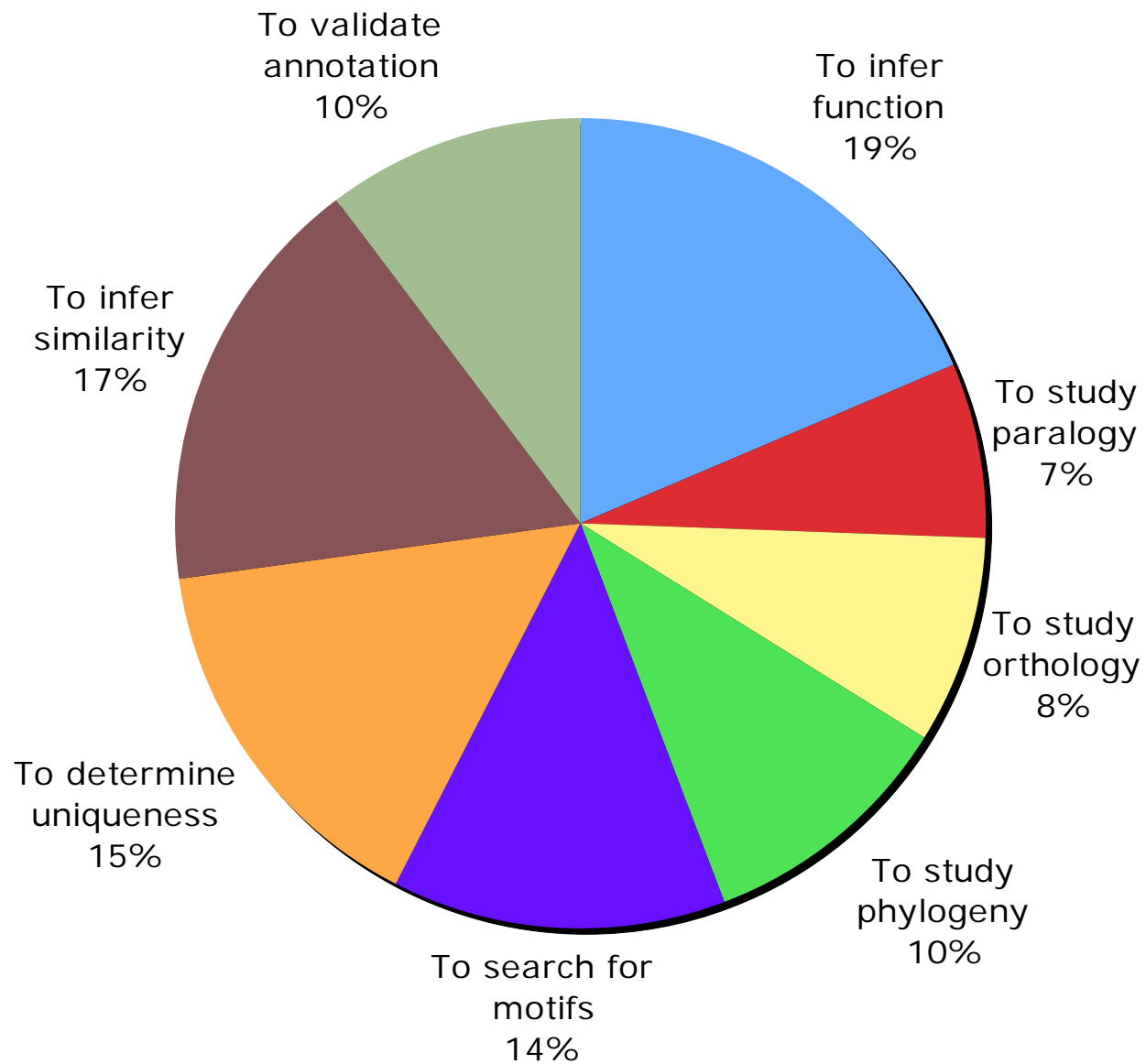


# Burkholderia Research Concerns

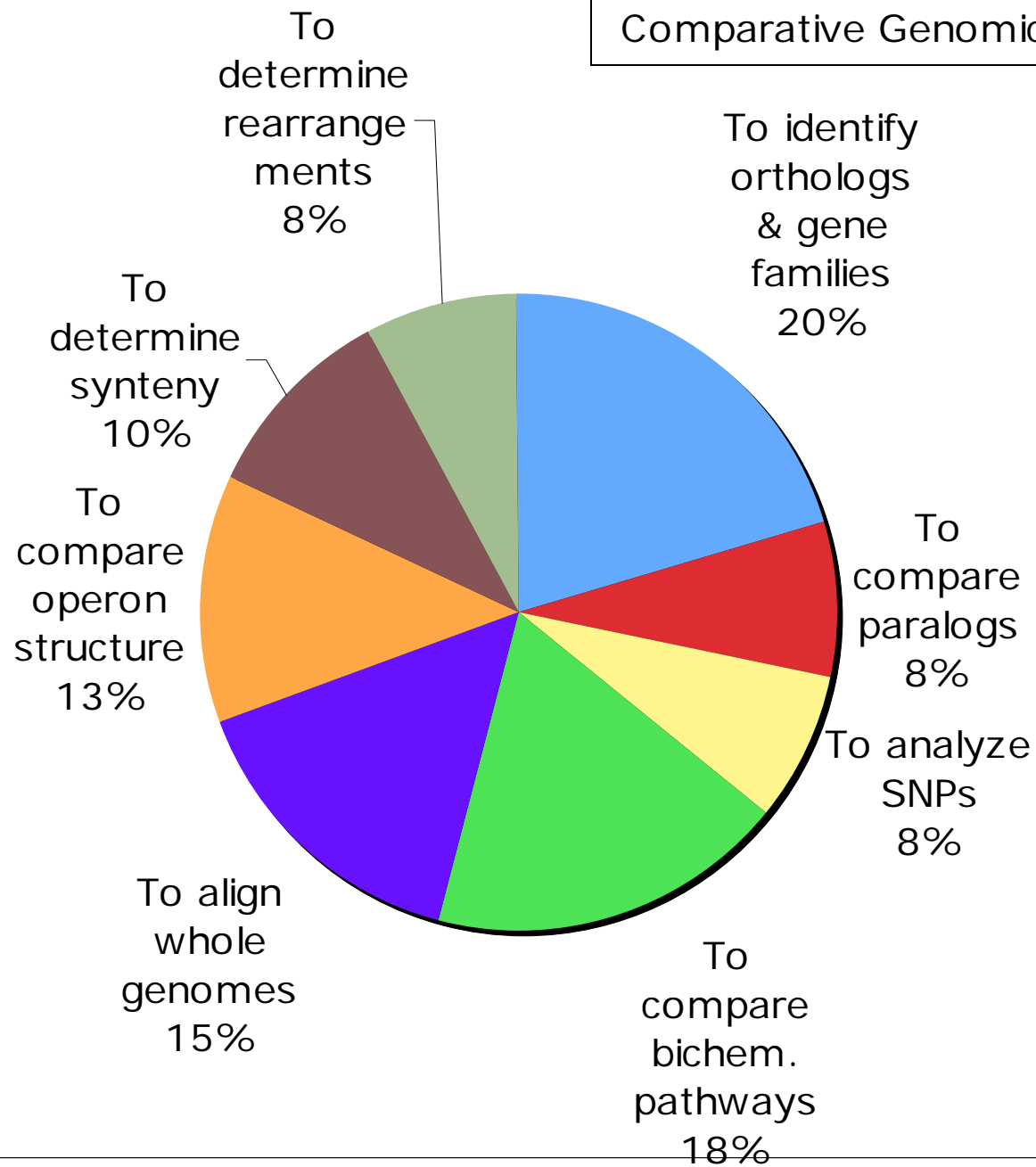




## Homology Searches



## Comparative Genomics





## Genome vs. Genome Protein Hits

**Comparing 2 genomes vs. reference genome with matches defined above 80% similarity**

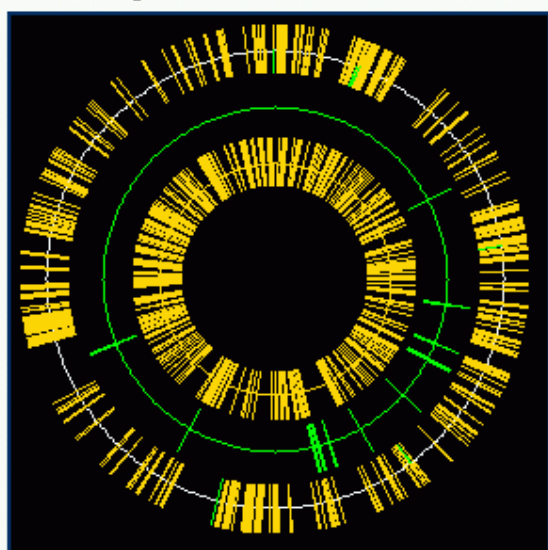


Image size: [Smaller](#) [Larger](#) [Huge](#)

This figure shows the protein matches of each comparison genome to the reference genome. Each ring of the circular display represents a genome and each tick mark represents a gene match along the length of the genome. The outer ring displays the reference genome and the inner rings display each comparison genome.

### Similarity cutoff for matches


☒ Above
 ☐ 40%
 ☐ 50%
 ☐ 60%
 ☐ 70%
 ☒ 80%
 ☐ 90%  
☐ Below Other:  %

### Reference Genome

Enterococcus faecalis V583

### Comparison Genomes

[Modify list](#)

 Haemophilus influenzae KW20

[14 genes match reference](#)

 Lactococcus lactis subsp. lactis IL1403

[333 genes match reference](#)

[347 total gene matches to reference genome](#)  
[Logic](#)

### Summary statistics for reference genome

[323 reference genes](#) match a comparison genome at least once for the given criteria [Logic](#)

[12 reference genes](#) match all comparison genomes for the given criteria [Logic](#)

[3011 reference genes](#) match none of the comparison genomes for the given criteria [Logic](#)

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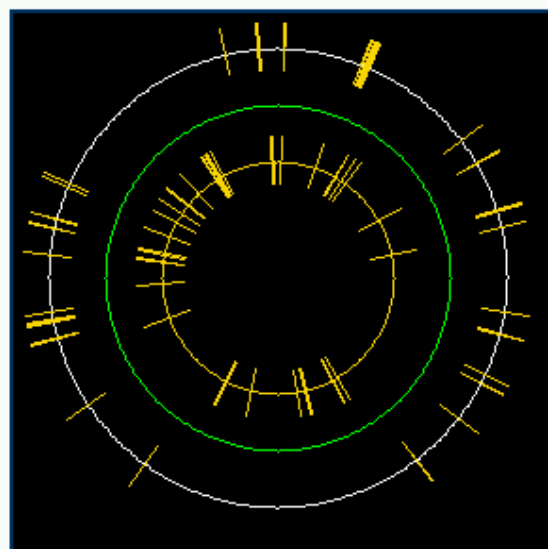


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## *Burkholderia* Survey Results

Number of Users: 29

QUESTION: 1. Which topics best apply to your current area of academic and research work

(Total:26)



Treatment [7.7% (2)]  
None [7.7% (2)]  
Vaccine Development [3.8% (1)]  
Host Cell Interactions: Host Immune responses [23.1% (6)]  
Detection & Identification of Organism [7.7% (2)]  
Molecular Epidemiology [7.7% (2)]  
Diagnostics [3.8% (1)]  
Pathogenesis [23.1% (6)]  
Host Cell Interactions: Antibiotic resistance [3.8% (1)]  
Prevention [3.8% (1)]  
Virulence [7.7% (2)]

QUESTION: 2. How often do you seek information on the following topics ?

**Antibodies**

(Total:29)



Not at all [3.4% (1)]  
Occasionally [48.3% (14)]  
Somewhat Frequently [17.2% (5)]  
Very Frequently [20.7% (6)]  
N/A [10.3% (3)]

**Vaccines**

(Total:28)



Not at all [17.9% (5)]  
Occasionally [35.7% (10)]  
Somewhat Frequently [25.0% (7)]  
Very Frequently [14.3% (4)]  
N/A [7.1% (2)]

**Inhibitors**

(Total:28)



Not at all [10.7% (3)]  
Occasionally [42.9% (12)]  
Somewhat Frequently [25.0% (7)]  
Very Frequently [14.3% (4)]



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## Burkholderia Strain List

### *Burkholderia pseudomallei* Strains

Strain	Sequencing Center	Original Source	Clinical Data	MLST
K96243	<a href="#">Sanger</a>	Sirirug Songsivilai	Isolated in 1996 from a 34 year old female diabetic patient at Khon Kaen hospital, northeast Thailand with a clinical history of short incubation, septicemic infection, and rapid progression to death.	<a href="#">ST 10</a>
1710a	<a href="#">TIGR</a>	Wellcome Unit, Bangkok	Isolated from blood culture in 1996 from a 52-year old male rice farmer with a new diagnosis of diabetes mellitus presenting to Sappasithprasong hospital, Ubon Ratchathani, NE Thailand. Disseminated disease (bacteremia plus lung and soft tissue involvement). Survived to discharge. Relapsed in 1999 (see below).	<a href="#">ST 177</a>
1710b	<a href="#">TIGR</a>	Wellcome Unit, Bangkok	Isolated from blood culture in March 1999 from patient described above. Died on day of admission.	<a href="#">ST 177</a>
1106a	<a href="#">TIGR</a>	Wellcome Unit, Bangkok	Isolated from pus aspirated from liver abscess in 1993 from a 23-year old female rice farmer presenting to Sappasithprasong hospital. Risk factors: thalassaemia and splenectomy. Multiple hepatic abscesses. Survived to discharge. Relapsed in 1996 (see below).	<a href="#">ST 70</a>
1106b	<a href="#">TIGR</a>	Wellcome Unit, Bangkok	Isolated from pus aspirated from liver abscess in 1996 from patient described above. Survived to discharge.	<a href="#">ST 70</a>
S13	<a href="#">TIGR</a>	Singapore	Mucoid environmental strain.	<a href="#">ST 51</a>
1655	<a href="#">TIGR</a>	Australia	From Menzies School of Health Research. 2003 sputum isolate from a 64 year old female patient from Darwin treated at Royal Darwin Hospital for chronic pulmonary melioidosis on a background of severe bronchiectasis.	<a href="#">ST 131</a>
668	<a href="#">TIGR</a>	Australia	From Menzies School of Health Research. 1995 blood culture isolate from a 53 year old male patient from Darwin with severe melioidosis encephalomyelitis. Required prolonged ventilation at Royal Darwin Hospital ICU but survived with good cognitive function but residual hemiparesis.	<a href="#">ST 129</a>
406e	<a href="#">TIGR</a>	Wellcome Unit, Bangkok	Isolated from toe swab in 1988 from a 21-year old male labourer presenting to Sappasithprasong hospital. Disseminated disease	<a href="#">ST 211</a>



## Primary Annotation Gene List ⓘ

*Burkholderia mallei* ATCC:23344

[Download](#)

Selected Annotation: Primary Annotation

[Add to Gene Cart](#)
[Select All](#)
[Clear All](#)

 1 – 250 of 5239 results | [next](#)

Cart	Locus	Gene Symbol	Common Name	EC Number	5' End	3' End	DNA molecule
<input type="checkbox"/>	<a href="#">BMA_0001</a>	dnaA	chromosomal replication initiator protein DnaA		25	1626	large chromosome <i>Burkholderia mallei</i> ATCC:23344
<input type="checkbox"/>	<a href="#">BMA_A0001</a>		hypothetical protein		1139	2326	small chromosome <i>Burkholderia mallei</i> ATCC:23344
<input type="checkbox"/>	<a href="#">BMA_0002</a>	dnaN	DNA polymerase III, beta subunit	<a href="#">2.7.7.7</a>	1789	2892	large chromosome <i>Burkholderia mallei</i> ATCC:23344
<input type="checkbox"/>	<a href="#">BMA_0003</a>	gyrB	DNA gyrase, B subunit	<a href="#">5.99.1.3</a>	3081	5549	large chromosome <i>Burkholderia mallei</i> ATCC:23344
<input type="checkbox"/>	<a href="#">BMA_A0002</a>		phage integrase family protein		3463	2420	small chromosome <i>Burkholderia mallei</i> ATCC:23344
<input type="checkbox"/>	<a href="#">BMA_A0003</a>		hypothetical protein		3955	3626	small chromosome <i>Burkholderia mallei</i> ATCC:23344
<input type="checkbox"/>	<a href="#">BMA_A0004</a>		DNA-binding protein		4694	4086	small chromosome <i>Burkholderia mallei</i> ATCC:23344
<input type="checkbox"/>	<a href="#">BMA_A0005</a>	kbl	2-amino-3-ketobutyrate coenzyme A ligase	<a href="#">2.3.1.29</a>	4862	6061	small chromosome <i>Burkholderia mallei</i> ATCC:23344
<input type="checkbox"/>	<a href="#">BMA_A0006</a>	tdh	L-threonine 3-dehydrogenase	<a href="#">1.1.1.103</a>	6074	7105	small chromosome <i>Burkholderia mallei</i> ATCC:23344



## Gene List By Evidence Type <sup>i</sup>

*Burkholderia mallei* ATCC:23344

Download

Selected Annotation: Primary Annotation

Selected Evidence Types: IDA, IMP

Add to Gene Cart

Select All

Clear All

1 - 5 of 5

Cart	Locus	Gene Symbol	Common Name	EC Number	5' End	3' End	Evidence Type: Function	Evidence Type: Process	DNA molecule
<input type="checkbox"/>	<a href="#">BMA_0315</a>		efflux transporter, RND family, MFP subunit		330873	332135	<a href="#">IDA</a>	<a href="#">IDA</a>	large chromosome <i>Burkholderia mallei</i> ATCC:23344
<input type="checkbox"/>	<a href="#">BMA_0316</a>		hydrophobe/amphiphile efflux family protein		332151	335351	<a href="#">IDA</a>	<a href="#">IDA</a>	large chromosome <i>Burkholderia mallei</i> ATCC:23344
<input type="checkbox"/>	<a href="#">BMA_2888</a>		acid phosphatase AcpA		2981117	2979384	<a href="#">IDA</a>	<a href="#">ND</a>	large chromosome <i>Burkholderia mallei</i> ATCC:23344
<input type="checkbox"/>	<a href="#">BMA_A1046</a>		RND efflux system, outer membrane lipoprotein, NodT family		1088036	1089574	<a href="#">IDA</a>	<a href="#">IDA</a>	small chromosome <i>Burkholderia mallei</i> ATCC:23344
<input type="checkbox"/>	<a href="#">BMA_A0749</a>		hemagglutinin domain protein		769356	768235	<a href="#">ND</a>	<a href="#">IMP</a>	small chromosome <i>Burkholderia mallei</i> ATCC:23344

# Trends

- Develop surrogates
- People really do participate in surveys
- Many solutions were simple



# Trends

- People really like:
  - Evidence
  - “experimentally determined” information
  - Publications
  - Protocols

# Soon

Rat Genome Database:

“How do I....” page.

# Next few months

## SWAT team custom analysis

- Email list and survey development defines responsive users
- Choose two
- Create situation-room
- Develop solution, walk user through
- Roll into interface
- Question: do people really need the interface?

Image: the BRC smokejumper